

*(Attachment #1)*

NCBI

## BLAST Search Results

BLAST

Entrez

[?]

BLASTN 2.1.1 [Aug-8-2000]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 971791677-8991-23542

**Query=**

(17 letters)

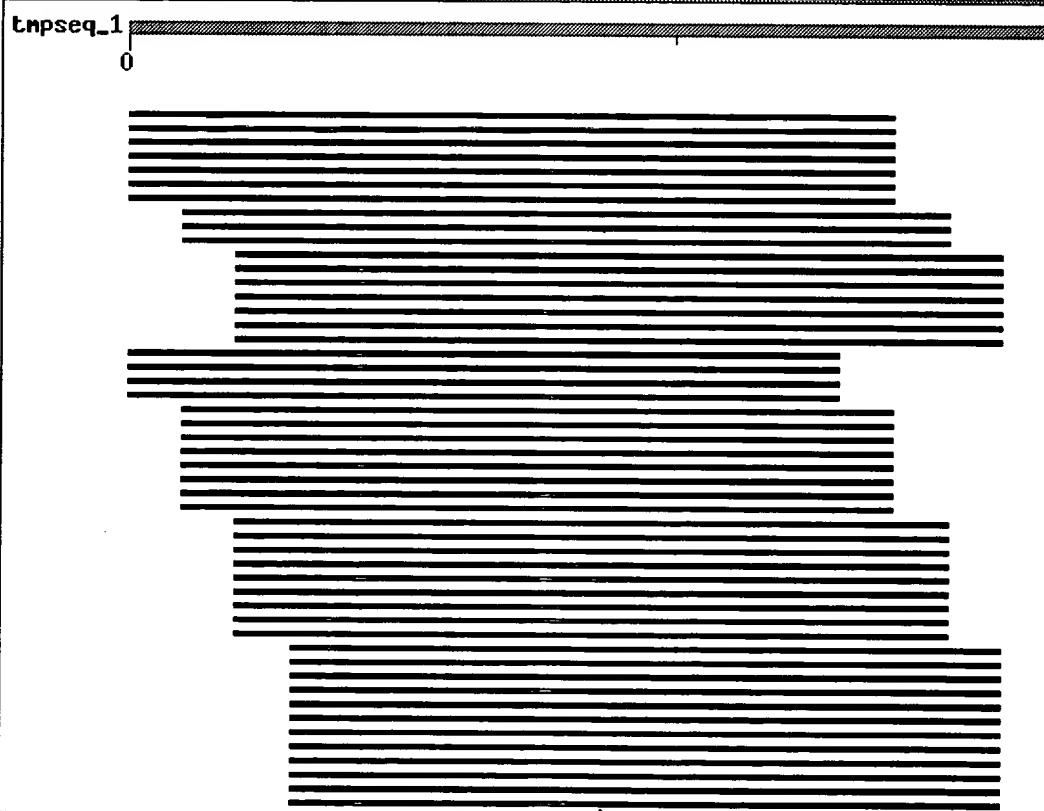
**Database:** nt

709,140 sequences; 2,366,395,475 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 66 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

			Score (bits)	E Value
gb AE003653.2 AE003653	Drosophila melanogaster genomic scaf...	30	1.9	
gb AC009890.12 AC009890	Genomic Sequence For Homo sapiens C...	30	1.9	
gb AC005099.1 AC005099	Homo sapiens BAC clone CTA-351J1 fro...	30	1.9	
gb AC005548.1 AC005548	Homo sapiens chromosome 17, clone hR...	30	1.9	
emb AL365229.13 AL365229	Human DNA sequence from clone RP11...	30	1.9	
gb AF022794.1 AF022794	Homo sapiens chromosome 21q22.2 cosm...	30	1.9	
gb AF020800.1 AF020800	Homo sapiens cosmid Q96E10 from the ...	30	1.9	
emb AL138831.12 AL138831	Human DNA sequence from clone RP3-...	30	1.9	
gb U80460.1 HSXIST2	Human Xq13 3' end of PAC 92E23 containi...	30	1.9	
emb AL163267.2 HS21C067	Homo sapiens chromosome 21 segment ...	30	1.9	
gb AF016420.1 CELC13D9	Caenorhabditis elegans cosmid C13D9	30	1.9	
emb AJ229042.1 HS229042	Homo sapiens 959 kb contig between ...	30	1.9	
emb AL024498.12 HS417M14	Human DNA sequence from clone RP3-...	30	1.9	
emb AL121578.1 HSXKSRPXR	Homo sapiens chromosome X sequence...	30	1.9	
emb AJ248285.1 CNSPAX03	Pyrococcus abyssi complete genome; ...	30	1.9	
dbj AB023039.1 AB023039	Arabidopsis thaliana genomic DNA, c...	30	1.9	
gb M35878.1 HUMIBP3	Human insulin-like growth factor-bindin...	30	1.9	
gb U18839.1 SCE9747	Saccharomyces cerevisiae chromosome V c...	28	7.4	
gb AE003442.1 AE003442	Drosophila melanogaster genomic scaf...	28	7.4	
gb AE003600.2 AE003600	Drosophila melanogaster genomic scaf...	28	7.4	
gb AC005283.2 AC005283	Homo sapiens PAC clone RP5-1039L24 f...	28	7.4	
gb AC074283.2 AC074283	Oryza sativa chromosome 10 clone OSJ...	28	7.4	
gb AC008639.7 AC008639	Homo sapiens chromosome 5 clone CTB-...	28	7.4	
gb AC016644.7 AC016644	Homo sapiens chromosome 5 clone RP11...	28	7.4	
gb AF121105.1 AF121105	Homo sapiens interleukin 16 gene, pa...	28	7.4	
ref NC_001137.2	Saccharomyces cerevisiae chromosome V, com...	28	7.4	
gb AC009075.6 AC009075	Homo sapiens chromosome 16 clone RP1...	28	7.4	
gb AF244084.1 AF244084	Edwardsiella ictaluri plasmid pEI2, ...	28	7.4	
gb AE002176.2 AE002176	Chlamydophila pneumoniae AR39, secti...	28	7.4	
gb AF254983.1 AF254983	Homo sapiens chromosome 21 clone BAC...	28	7.4	
gb AC003078.1 AC003078	Human BAC clone GS1-117010 from 7q21...	28	7.4	
ref NM_007584.1	Mus musculus cell adhesion kinase (Cak), mRNA	28	7.4	
gb AC004682.1 HUAC004682	Homo sapiens Chromosome 16 BAC clo...	28	7.4	
gb AC007207.22 AC007207	Homo sapiens 12p13.3-4.6-10.5 BAC R...	28	7.4	
ref NC_001778.1	Polypterus ornatipinnis mitochondrial, com...	28	7.4	
gb AE001644.1 AE001644	Chlamydia pneumoniae section 60 of 1...	28	7.4	
gb AC006287.1 AC006287	Homo sapiens, clone hRPK.22_A_1, com...	28	7.4	
gb AC003019.1 AC003019	Mus musculus Chromosome 4 BAC clone ...	28	7.4	
gb AC005888.1 AC005888	Homo sapiens 12q24.2 PAC RPCI1-116K2...	28	7.4	
gb AC005808.1 AC005808	Homo sapiens chromosome 20, P1 clone...	28	7.4	
gb U62532.1 POU62532	Polypterus ornatipinnis, complete mitoc...	28	7.4	
gb AC002366.1 AC002366	Human Xp22 BAC CT-285I15 (from CalTe...	28	7.4	
emb AL139087.13 AL139087	Human DNA sequence from clone RP11...	28	7.4	
emb AL157838.24 AL157838	Human DNA sequence from clone RP4-...	28	7.4	
emb AL137067.7 AL137067	Human DNA sequence from clone RP11-...	28	7.4	
emb AL158167.15 AL158167	Human DNA sequence from clone RP11...	28	7.4	
emb AX012403.1 AX012403	Sequence 4 from Patent EP0955363	28	7.4	
emb AL163201.2 HS21C001	Homo sapiens chromosome 21 segment ...	28	7.4	
emb AL158043.14 AL158043	Human DNA sequence from clone RP11...	28	7.4	
gb AF026259.1 AF026259	Mus musculus receptor-like tyrosine ...	28	7.4	
emb AL118508.27 HSJ737E23	Human DNA sequence from clone RP4...	28	7.4	
emb AL161669.3 CNS01RHC	Human chromosome 14 DNA sequence **...	28	7.4	
emb AL135747.2 CNS01DVE	Human chromosome 14 DNA sequence **...	28	7.4	
emb AL133241.3 CNS01DUE	Human chromosome 14 DNA sequence **...	28	7.4	
emb AL162755.2 NMA4Z22491	Neisseria meningitidis serogroup A...	28	7.4	
gb L07554.1 LINPEROX	Linum usitatissimum peroxidase (FLXPER...	28	7.4	
emb AL033397.7 HS27K12	Human DNA sequence from clone 27K12 ...	28	7.4	
emb AL023655.1 HS242N11	Human DNA sequence from clone 242N1...	28	7.4	
emb AL078476.2 HSB7L1C4	Homo sapiens chromosome 21 BAC B7L1...	28	7.4	
dbj AP002547.2 AP002547	Chlamydophila pneumoniae genomic DN...	28	7.4	

## Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

gb AE003653.2 AE003653	Drosophila melanogaster genomic scaf...	30	1.9
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gb AC005548.1 AC005548	Homo sapiens chromosome 17, clone hR...	30	1.9
emb AL365229.13 AL365229	Human DNA sequence from clone RP11...	30	1.9
gb AF022794.1 AF022794	Homo sapiens chromosome 21q22.2 cosm...	30	1.9
gb AF020800.1 AF020800	Homo sapiens cosmid Q96E10 from the ...	30	1.9
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gb U80460.1 HSXIST2	Human Xq13 3' end of PAC 92E23 containi...	30	1.9
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gb AF016420.1 CELC13D9	Caenorhabditis elegans cosmid C13D9	30	1.9
emb AJ229042.1 HS229042	Homo sapiens 959 kb contig between ...	30	1.9
emb AL024498.12 HS417M14	Human DNA sequence from clone RP3-...	30	1.9
emb AL121578.1 HSXKSRPXR	Homo sapiens chromosome X sequence...	30	1.9
emb AJ248285.1 CNSPAX03	Pyrococcus abyssi complete genome; ...	30	1.9
dbj AB023039.1 AB023039	Arabidopsis thaliana genomic DNA, c...	30	1.9
gb M35878.1 HUMIBP3	Human insulin-like growth factor-bindin...	30	1.9
gb U18839.1 SCE9747	Saccharomyces cerevisiae chromosome V c...	28	7.4
gb AE003442.1 AE003442	Drosophila melanogaster genomic scaf...	28	7.4
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gb AC074283.2 AC074283	Oryza sativa chromosome 10 clone OSJ...	28	7.4
gb AC008639.7 AC008639	Homo sapiens chromosome 5 clone CTB-...	28	7.4
gb AC016644.7 AC016644	Homo sapiens chromosome 5 clone RP11...	28	7.4
gb AF121105.1 AF121105	Homo sapiens interleukin 16 gene, pa...	28	7.4
ref NC_001137.2	Saccharomyces cerevisiae chromosome V, com...	28	7.4
gb AC009075.6 AC009075	Homo sapiens chromosome 16 clone RP1...	28	7.4
gb AF244084.1 AF244084	Edwardsiella ictaluri plasmid PEI2, ...	28	7.4
gb AE002176.2 AE002176	Chlamydophila pneumoniae AR39, secti...	28	7.4
gb AF254983.1 AF254983	Homo sapiens chromosome 21 clone BAC...	28	7.4
gb AC003078.1 AC003078	Human BAC clone GS1-117010 from 7q21...	28	7.4
ref NM_007584.1	Mus musculus cell adhesion kinase (Cak), mRNA	28	7.4
gb AC004682.1 HUAC004682	Homo sapiens Chromosome 16 BAC clo...	28	7.4
gb AC007207.22 AC007207	Homo sapiens 12p13.3-4.6-10.5 BAC R...	28	7.4
ref NC_001778.1	Polypterus ornatipinnis mitochondrion, com...	28	7.4
gb AE001644.1 AE001644	Chlamydia pneumoniae section 60 of 1...	28	7.4
gb AC006287.1 AC006287	Homo sapiens, clone hRPK.22_A_1, com...	28	7.4
gb AC003019.1 AC003019	Mus musculus Chromosome 4 BAC clone ...	28	7.4
gb AC005888.1 AC005888	Homo sapiens 12q24.2 PAC RPCII-116K2...	28	7.4
gb AC005808.1 AC005808	Homo sapiens chromosome 20, P1 clone...	28	7.4
gb U62532.1 POU62532	Polypterus ornatipinnis complete mitoc...	28	7.4
gb AC002366.1 AC002366	Human Xp22 BAC CT-285I15 (from CalTe...	28	7.4
emb AL139087.13 AL139087	Human DNA sequence from clone RP11...	28	7.4
emb AL157838.24 AL157838	Human DNA sequence from clone RP4-...	28	7.4
emb AL137067.7 AL137067	Human DNA sequence from clone RP11-...	28	7.4
emb AL158167.15 AL158167	Human DNA sequence from clone RP11...	28	7.4
emb AX012403.1 AX012403	Sequence 4 from Patent EP0955363	28	7.4
emb AL163201.2 HS21C001	Homo sapiens chromosome 21 segment ...	28	7.4
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gb AF026259.1 AF026259	Mus musculus receptor-like tyrosine ...	28	7.4
emb AL118508.27 HSJ737E23	Human DNA sequence from clone RP4...	28	7.4
emb AL161669.3 CNS01RHC	Human chromosome 14 DNA sequence **...	28	7.4
emb AL135747.2 CNS01DVE	Human chromosome 14 DNA sequence **...	28	7.4
emb AL133241.3 CNS01DUE	Human chromosome 14 DNA sequence **...	28	7.4
emb AL162755.2 NMA4Z22491	Neisseria meningitidis serogroup A...	28	7.4
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emb AL023655.1 HS242N11	Human DNA sequence from clone 242N1...	28	7.4
emb AL078476.2 HSB7L1C4	Homo sapiens chromosome 21 BAC B7L1...	28	7.4
dbj AP002547.2 AP002547	Chlamydophila pneumoniae genomic DN...	28	7.4

<u>gb L57509.1 MUSCAK</u>	Mus musculus Cak receptor kinase mRNA, c...	<u>28</u>	7.4
<u>dbj AB026898.1 AB026898</u>	Homo sapiens DNA, DLEC1 to ORCTL4 g...	<u>28</u>	7.4
<u>dbj D64000.1 SYCSLRB</u>	Synechocystis sp. PCC6803 complete gen...	<u>28</u>	7.4
<u>emb Y10466.1 SOPRXR5</u>	S.oleracea mRNA for peroxidase, clone ...	<u>28</u>	7.4
<u>dbj AP000499.1 AP000499</u>	Homo sapiens genomic DNA, chromosom...	<u>28</u>	7.4
<u>gb L26525.1 RATPTK3D</u>	Rattus norvegicus tyrosine kinase rece...	<u>28</u>	7.4

### Alignments

>gb|AE003653.2|AE003653 Drosophila melanogaster genomic scaffold 142000013386055 :  
of 63, complete sequence  
Length = 249469

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 2 aattaggatgggaa 16  
|||||||||||||||  
Sbjct: 2445 aattaggatgggaa 2459

>gb|AC009890.12|AC009890 Genomic Sequence For Homo sapiens Clone H\_NH0262L04 From  
complete sequence  
Length = 177223

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 1 gaattaggatgggaa 15  
|||||||||||||||  
Sbjct: 142165 gaattaggatgggaa 142151

>gb|AC005099.1|AC005099 Homo sapiens BAC clone CTA-351J1 from 7q22-q31, complete :  
Length = 131611

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatgggaaa 17  
|||||||||||||||  
Sbjct: 70042 attaggatgggaaa 70028

>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756\_K\_11, complete  
Length = 156811

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 1 gaattaggatgggaa 15  
|||||||||||||||  
Sbjct: 133477 gaattaggatgggaa 133491

>emb|AL365229.13|AL365229 Human DNA sequence from clone RP11-723K16 on chromosome  
sequence [Homo sapiens]  
Length = 121478

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)

<u>gb L57509.1 MUSCAK</u>	Mus musculus Cak receptor kinase mRNA, c...	<u>28</u>	<u>7.4</u>
<u>dbj AB026898.1 AB026898</u>	Homo sapiens DNA, DLECl to ORCTL4 g...	<u>28</u>	<u>7.4</u>
<u>dbj D64000.1 SYCSLRB</u>	Synechocystis sp. PCC6803 complete gen...	<u>28</u>	<u>7.4</u>
<u>emb Y10466.1 SOPRXR5</u>	S.oleracea mRNA for peroxidase, clone ...	<u>28</u>	<u>7.4</u>
<u>dbj AP000499.1 AP000499</u>	Homo sapiens genomic DNA, chromosom...	<u>28</u>	<u>7.4</u>
<u>gb L26525.1 RATPTK3D</u>	Rattus norvegicus tyrosine kinase rece...	<u>28</u>	<u>7.4</u>

### Alignments

>gb|AE003653.2|AE003653 Drosophila melanogaster genomic scaffold 142000013386055 :  
of 63, complete sequence  
Length = 249469

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 2 aattaggatggggaa 16  
|||||||||||||||  
Sbjct: 2445 aattaggatggggaa 2459

>gb|AC009890.12|AC009890 Genomic Sequence For Homo sapiens Clone H\_NH0262L04 From  
complete sequence  
Length = 177223

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 1 gaattaggatgggga 15  
|||||||||||||||  
Sbjct: 142165 gaattaggatgggga 142151

>gb|AC005099.1|AC005099 Homo sapiens BAC clone CTA-351J1 from 7q22-q31, complete :  
Length = 131611

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatgggaaa 17  
|||||||||||||||  
Sbjct: 70042 attaggatgggaaa 70028

>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756\_K\_11, complete  
Length = 156811

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 1 gaattaggatgggga 15  
|||||||||||||||  
Sbjct: 133477 gaattaggatgggga 133491

>emb|AL365229.13|AL365229 Human DNA sequence from clone RP11-723K16 on chromosome  
sequence [Homo sapiens]  
Length = 121478

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)

Strand = Plus / Plus

Query: 1        gaatttaggatgggga 15

|||||||||||||||

Sbjct: 58988 gaatttaggatgggga 59002

>gb|AF022794.1|AF022794 Homo sapiens chromosome 21q22.2 cosmid Q80D10, complete sequence  
Length = 44897

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 3        attaggatggggaaa 17

|||||||||||||||

Sbjct: 14979 attaggatggggaaa 14965

>gb|AF020800.1|AF020800 Homo sapiens cosmid Q96E10 from the Down Syndrome critical region  
chromosome 21q22.2, complete sequence  
Length = 41075

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 3        attaggatggggaaa 17

|||||||||||||||

Sbjct: 39162 attaggatggggaaa 39148

>emb|AL138831.12|AL138831 Human DNA sequence from clone RP3-406P24 on chromosome 1  
sequence [Homo sapiens]  
Length = 49600

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 1        gaatttaggatgggga 15

|||||||||||||||

Sbjct: 17231 gaatttaggatgggga 17217

>gb|U80460.1|HSXIST2 Human Xq13 3' end of PAC 92E23 containing the X inactivation  
(XIST) gene, complete sequence [Homo sapiens]  
Length = 135886

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Plus

Query: 2        aatttaggatggggaa 16

|||||||||||||||

Sbjct: 36978 aatttaggatggggaa 36992

>emb|AL163267.2|HS21C067 Homo sapiens chromosome 21 segment HS21C067  
Length = 340000

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Plus

Strand = Plus / Plus

Query: 1        gaatttaggatgggga 15

|||||||||||||||

Sbjct: 58988 gaatttaggatgggga 59002

>gb|AF022794.1|AF022794 Homo sapiens chromosome 21q22.2 cosmid Q80D10, complete sequence  
Length = 44897

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 3        attaggatgggaaa 17

|||||||||||||||

Sbjct: 14979 attaggatgggaaa 14965

>gb|AF020800.1|AF020800 Homo sapiens cosmid Q96E10 from the Down Syndrome critical region of chromosome 21q22.2, complete sequence  
Length = 41075

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 3        attaggatgggaaa 17

|||||||||||||||

Sbjct: 39162 attaggatgggaaa 39148

>emb|AL138831.12|AL138831 Human DNA sequence from clone RP3-406P24 on chromosome 12, complete sequence [Homo sapiens]  
Length = 49600

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Minus

Query: 1        gaatttaggatgggga 15

|||||||||||||||

Sbjct: 17231 gaatttaggatgggga 17217

>gb|U80460.1|HSXIST2 Human Xq13 3' end of PAC 92E23 containing the X inactivation (XIST) gene, complete sequence [Homo sapiens]  
Length = 135886

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Plus

Query: 2        aatttaggatgggaaa 16

|||||||||||||||

Sbjct: 36978 aatttaggatgggaaa 36992

>emb|AL163267.2|HS21C067 Homo sapiens chromosome 21 segment HS21C067  
Length = 340000

Score = 30.2 bits (15), Expect = 1.9

Identities = 15/15 (100%)

Strand = Plus / Plus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 253757 attaggatggggaaa 253771

>gb|AF016420.1|CELC13D9 Caenorhabditis elegans cosmid C13D9  
Length = 43487

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 1 gaatttaggatgggga 15  
|||||||||||||||  
Sbjct: 24516 gaatttaggatgggga 24530

>emb|AJ229042.1|HS229042 Homo sapiens 959 kb contig between AML1 and CBR1 on chro  
segment 2/3  
Length = 348050

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 284320 attaggatggggaaa 284306

>emb|AL024498.12|HS417M14 Human DNA sequence from clone RP3-417M14 on chromosome 1  
Contains a novel gene, the gene for a novel  
serine/threonine-protein kinase (ortholog of mouse and rat  
MAK (male germ cell-associated kinase), the 3' end of the  
GCMB gene for glial cells>  
Length = 144186

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 79114 attaggatggggaaa 79100

>emb|AL121578.1|HSXKSRPXR Homo sapiens chromosome X sequence from 12 cosmids, map  
DXS709-SRPX, complete sequence  
Length = 337101

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 40278 attaggatggggaaa 40264

>emb|AJ248285.1|CNSPAX03 Pyrococcus abyssi complete genome; segment 3/6  
Length = 307120

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 253757 attaggatggggaaa 253771

>gb|AF016420.1|CELC13D9 Caenorhabditis elegans cosmid C13D9  
Length = 43487

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Plus

Query: 1 gaatttaggatgggga 15  
|||||||||||||||  
Sbjct: 24516 gaatttaggatgggga 24530

>emb|AJ229042.1|HS229042 Homo sapiens 959 kb contig between AML1 and CBR1 on chro  
segment 2/3  
Length = 348050

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 284320 attaggatggggaaa 284306

>emb|AL024498.12|HS417M14 Human DNA sequence from clone RP3-417M14 on chromosome 6  
Contains a novel gene, the gene for a novel  
serine/threonine-protein kinase (ortholog of mouse and rat  
MAK (male germ cell-associated kinase), the 3' end of the  
GCMB gene for glial cells>  
Length = 144186

Score = 30.2 bits (15), Expect = 1.9  
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Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 79114 attaggatggggaaa 79100

>emb|AL121578.1|HSXKSRPXR Homo sapiens chromosome X sequence from 12 cosmids, map  
DXS709-SRPX, complete sequence  
Length = 337101

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus

Query: 3 attaggatggggaaa 17  
|||||||||||||||  
Sbjct: 40278 attaggatggggaaa 40264

>emb|AJ248285.1|CNSPAX03 Pyrococcus abyssi complete genome; segment 3/6  
Length = 307120

Score = 30.2 bits (15), Expect = 1.9  
Identities = 15/15 (100%)  
Strand = Plus / Minus